SEQUENCE LISTING

<110> Allen, Keith D.

<120> TRANSGENIC MICE CONTAINING CALCIUM ION CHANNEL (Trp6) GENE DISRUPTIONS

<130> R-881

<150> US 60/280,373
<151> 2001-03-29

<150> US 60/255,227
<151> 2000-12-11

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3261
<212> DNA
<213> Mus musculus

<400> 1
cgcctgtgcc ctctgcctgg gagcctgggg ccgcctgtct gcgcggtccg gatgcgctca 60
ggtcaaggtt cctttcgcgg ctgtctccca agcccctaac tagtgacttc cactgtggcg 120
ggcagggaag ccattggcag aacctagcca gtcaggaatc tgcatctctt ccctcattat 180
cctctccctg gcattgcttt gctcgggtcc agctcagttg gtgacgcggc cccttctccc 240
caggttggga tccacggaag caggggtgca ggccggccag gcactgtgcc atgagccaga 300
gcccgaggtt cgtgacccgg aggggcggct ctctaaaggc tgcccctgga gccggcaccc 360
ggcgcaacga gagccaggac tatttgctga tggacgagct gggagacgac ggctacccgc 420
agctcccgct gccaccgtat ggctactacc ccagcttccg gggtaatgaa aacagactga 480
ctcaccggcg gcagacgatt cttcgtgaga agggaagaag gttagctaat cgaggaccag 540
catacatgtt taatgatcat tcaacaagcc tgtctattga ggaagaacgc tttctagatg 600
cagttgaata tggcaacatc ccagtggtct ggaagatgct agaagagtgt cattccctca 660
atgttaactg tgtggattac atgggccaga atgccctaca gctggctgtg gccaatgagc 720
acttggaaat cacagagctg ctactcaaga aggaaaactt gtctcgagtt ggggatgctt 780
tacttttagc cattagtaaa ggttatgtac ggattgtgga ggcaatcctc aaccatccat 840
cttttgctga aggcaaaagg ttagcgacaa gccccagcca gtctgaactt cagcaagatg 900
actttttatgc ctatgatgaa gatgggacgc ggttctccca tgatgtgact ccaatcattc 960
tcgctgcaca ttgccaggaa tatgaaattg tgcataccct cctgagaaag ggtgcccgga 1020
ttgagcggcc tcatgattac ttctgcaagt gtacagaatg cagccagaag cagaagcatg 1080
attccttcag ccactctaga tccaggatca atgcatacaa aggtctggca agtccagcat 1140
acctgtcatt gtccagtgaa gatccagtca tgactgcttt agaacttagc aatgagctgg 1200
cagtgcttgc caacattgag aaagagttca agaatgacta caggaagctg tctatgcagt 1260
gcaaggattt cgttgttggt ctcttggacc tctgcagaaa cacagaggaa gtggaggcca 1320
tcctgaatgg ggatgcagag actcgccagc ccggggactt cggccgtcca aatctcagcc 1380
gtttaaaact tgctattaag gatgaagtaa aaaaatttgt ggctcatcca aactgtcagc 1440
aacagctcct gtccatatgg tatgagaacc tctctggttt acggcagcag accatggcag 1500
tgaagttcct cgtggtcctt gctgttgcca ttggattgcc cttcctggct ctcatatact 1560
ggtgtgctcc ttgcagcaag atggggaaga tattgccgag accgttcatg aagtttgtag 1620
cacacgcagc ctccttcacc attttcctgg ggctgctcgt catgaatgca gctgacagat 1680
ttgaaggcac caagctcctc cctaatgaaa ccagcacaga taatgcaagg cagctgttca 1740
ggatgaaaac atcctgtttc tcatggatgg agatgctcat tatatcctgg gtaataggca 1800
tgatatgggc tgaatgtaaa gaaatctgga ctcaaggccc caaagaatac ttatttgagt 1860
tgtggaatat gcttgacttt ggaatgctgg caatctttgc agcatcattc attgcaagat 1920
ttatggcgtt ctggcatgca tccaaagctc agagcatcat tgatgcaaat gatactttaa 1980
aggatttgac aaaagtcaca ctgggggaca acgttaaata ctacaatctg gccaggataa 2040

```
agtgggaccc tactgatcct cagatcatct ctgaaggtct ttatgcaatc gctgtggttt 2100
taagtttctc cagaatagct tacattttac cagcaaatga aagctttgga cctctgcaga 2160
tttcacttgg aagaacagtg aaagatatct tcaaattcat ggtcatattc atcatggtgt 2220
ttgtagcctt tatgattgga atgttcaacc tttactccta ctacattggc gcaaaacaga 2280
atgaagcatt cacaacagtt gaggaaagtt ttaagacact gttctgggct atctttggtc 2340
tttctgaagt gaagtcagtg gtcattaact acaatcacaa gttcattgaa aacatcggct 2400
acgttctgta tggtgtctat aatgtcacaa tggtcattgt tttgctaaat atgttaattg 2460
cgatgatcaa tagttcattc caggaaattg aggatgatgc ggacgtggag tggaagtttg 2520
caagggccaa attgtggttt tcctactttg aggaggggag aacacttcct gtccccttca 2580
atcttgtacc aagtccaaaa tccttgcttt atctcctatt gaaatttaag aaatggatgt 2640
gtgagctcat ccagggtcaa aagcaaggct tccaagaaga tgcagagatg aacaagagaa 2700
atgaagaaaa gaaatttgga atttcaggaa gtcacgaaga cctttcaaaa ttttcacttg 2760
acaaaaatca gttggcacac aacaaacaat caagtacaag gagctcagaa gattatcatt 2820
taaatagttt cagtaaccct ccaagacaat atcagaaaat catgaagaga ctcattaaaa 2880
gatatgtatt gcaggcccag attgataagg agagcgatga ggtgaatgaa ggggaattga 2940
aggaaattaa gcaagacatc tcaagtctcc gttatgaact ccttgaagag aaatcacaga 3000
actcagaaga cctagcagag ctcattagaa aactcgggga gagactgtcg ttagagccaa 3060
agctggagga aagccgcaga tagagcagag cccctcagaa gtgcatattt atttctccac 3120
ttgaagccat attattttct gacttatttt tttaagtgtc aatgataaaa agtatgttaa 3180
ctgataactt ggatcattta gagtcctaat atcaagcttt ttgggagatt aaattgcatt 3240
gctgagggct aacaattgct g                                          3261
```

<210> 2
<211> 930
<212> PRT
<213> Mus musculus

<400> 2

```
Met Ser Gln Ser Pro Arg Phe Val Thr Arg Arg Gly Gly Ser Leu Lys
 1               5                  10                  15
Ala Ala Pro Gly Ala Gly Thr Arg Arg Asn Glu Ser Gln Asp Tyr Leu
            20                  25                  30
Leu Met Asp Glu Leu Gly Asp Asp Gly Tyr Pro Gln Leu Pro Leu Pro
        35                  40                  45
Pro Tyr Gly Tyr Tyr Pro Ser Phe Arg Gly Asn Glu Asn Arg Leu Thr
    50                  55                  60
His Arg Arg Gln Thr Ile Leu Arg Glu Lys Gly Arg Arg Leu Ala Asn
65                  70                  75                  80
Arg Gly Pro Ala Tyr Met Phe Asn Asp His Ser Thr Ser Leu Ser Ile
                85                  90                  95
Glu Glu Glu Arg Phe Leu Asp Ala Val Glu Tyr Gly Asn Ile Pro Val
            100                 105                 110
Val Trp Lys Met Leu Glu Glu Cys His Ser Leu Asn Val Asn Cys Val
        115                 120                 125
Asp Tyr Met Gly Gln Asn Ala Leu Gln Leu Ala Val Ala Asn Glu His
    130                 135                 140
Leu Glu Ile Thr Glu Leu Leu Leu Lys Lys Glu Asn Leu Ser Arg Val
145                 150                 155                 160
Gly Asp Ala Leu Leu Leu Ala Ile Ser Lys Gly Tyr Val Arg Ile Val
                165                 170                 175
Glu Ala Ile Leu Asn His Pro Ser Phe Ala Glu Gly Lys Arg Leu Ala
            180                 185                 190
Thr Ser Pro Ser Gln Ser Glu Leu Gln Gln Asp Asp Phe Tyr Ala Tyr
        195                 200                 205
Asp Glu Asp Gly Thr Arg Phe Ser His Asp Val Thr Pro Ile Ile Leu
    210                 215                 220
Ala Ala His Cys Gln Glu Tyr Glu Ile Val His Thr Leu Leu Arg Lys
225                 230                 235                 240
Gly Ala Arg Ile Glu Arg Pro His Asp Tyr Phe Cys Lys Cys Thr Glu
                245                 250                 255
Cys Ser Gln Lys Gln Lys His Asp Ser Phe Ser His Ser Arg Ser Arg
```

```
                260                 265                 270
Ile Asn Ala Tyr Lys Gly Leu Ala Ser Pro Ala Tyr Leu Ser Leu Ser
        275                 280                 285
Ser Glu Asp Pro Val Met Thr Ala Leu Glu Leu Ser Asn Glu Leu Ala
    290                 295                 300
Val Leu Ala Asn Ile Glu Lys Glu Phe Lys Asn Asp Tyr Arg Lys Leu
305                 310                 315                 320
Ser Met Gln Cys Lys Asp Phe Val Val Gly Leu Leu Asp Leu Cys Arg
                325                 330                 335
Asn Thr Glu Glu Val Glu Ala Ile Leu Asn Gly Asp Ala Glu Thr Arg
            340                 345                 350
Gln Pro Gly Asp Phe Gly Arg Pro Asn Leu Ser Arg Leu Lys Leu Ala
        355                 360                 365
Ile Lys Asp Glu Val Lys Lys Phe Val Ala His Pro Asn Cys Gln Gln
    370                 375                 380
Gln Leu Leu Ser Ile Trp Tyr Glu Asn Leu Ser Gly Leu Arg Gln Gln
385                 390                 395                 400
Thr Met Ala Val Lys Phe Leu Val Val Leu Ala Val Ala Ile Gly Leu
                405                 410                 415
Pro Phe Leu Ala Leu Ile Tyr Trp Cys Ala Pro Cys Ser Lys Met Gly
            420                 425                 430
Lys Ile Leu Pro Arg Pro Phe Met Lys Phe Val Ala His Ala Ala Ser
        435                 440                 445
Phe Thr Ile Phe Leu Gly Leu Leu Val Met Asn Ala Ala Asp Arg Phe
    450                 455                 460
Glu Gly Thr Lys Leu Leu Pro Asn Glu Thr Ser Thr Asp Asn Ala Arg
465                 470                 475                 480
Gln Leu Phe Arg Met Lys Thr Ser Cys Phe Ser Trp Met Glu Met Leu
                485                 490                 495
Ile Ile Ser Trp Val Ile Gly Met Ile Trp Ala Glu Cys Lys Glu Ile
            500                 505                 510
Trp Thr Gln Gly Pro Lys Glu Tyr Leu Phe Glu Leu Trp Asn Met Leu
        515                 520                 525
Asp Phe Gly Met Leu Ala Ile Phe Ala Ala Ser Phe Ile Ala Arg Phe
    530                 535                 540
Met Ala Phe Trp His Ala Ser Lys Ala Gln Ser Ile Ile Asp Ala Asn
545                 550                 555                 560
Asp Thr Leu Lys Asp Leu Thr Lys Val Thr Leu Gly Asp Asn Val Lys
                565                 570                 575
Tyr Tyr Asn Leu Ala Arg Ile Lys Trp Asp Pro Thr Asp Pro Gln Ile
            580                 585                 590
Ile Ser Glu Gly Leu Tyr Ala Ile Ala Val Val Leu Ser Phe Ser Arg
        595                 600                 605
Ile Ala Tyr Ile Leu Pro Ala Asn Glu Ser Phe Gly Pro Leu Gln Ile
    610                 615                 620
Ser Leu Gly Arg Thr Val Lys Asp Ile Phe Lys Phe Met Val Ile Phe
625                 630                 635                 640
Ile Met Val Phe Val Ala Phe Met Ile Gly Met Phe Asn Leu Tyr Ser
                645                 650                 655
Tyr Tyr Ile Gly Ala Lys Gln Asn Glu Ala Phe Thr Thr Val Glu Glu
            660                 665                 670
Ser Phe Lys Thr Leu Phe Trp Ala Ile Phe Gly Leu Ser Glu Val Lys
        675                 680                 685
Ser Val Val Ile Asn Tyr Asn His Lys Phe Ile Glu Asn Ile Gly Tyr
    690                 695                 700
Val Leu Tyr Gly Val Tyr Asn Val Thr Met Val Ile Val Leu Leu Asn
705                 710                 715                 720
Met Leu Ile Ala Met Ile Asn Ser Ser Phe Gln Glu Ile Glu Asp Asp
                725                 730                 735
Ala Asp Val Glu Trp Lys Phe Ala Arg Ala Lys Leu Trp Phe Ser Tyr
            740                 745                 750
```

Phe Glu Glu Gly Arg Thr Leu Pro Val Pro Phe Asn Leu Val Pro Ser
755 760 765
Pro Lys Ser Leu Leu Tyr Leu Leu Leu Lys Phe Lys Lys Trp Met Cys
770 775 780
Glu Leu Ile Gln Gly Gln Lys Gln Gly Phe Gln Glu Asp Ala Glu Met
785 790 795 800
Asn Lys Arg Asn Glu Glu Lys Lys Phe Gly Ile Ser Gly Ser His Glu
805 810 815
Asp Leu Ser Lys Phe Ser Leu Asp Lys Asn Gln Leu Ala His Asn Lys
820 825 830
Gln Ser Ser Thr Arg Ser Ser Glu Asp Tyr His Leu Asn Ser Phe Ser
835 840 845
Asn Pro Pro Arg Gln Tyr Gln Lys Ile Met Lys Arg Leu Ile Lys Arg
850 855 860
Tyr Val Leu Gln Ala Gln Ile Asp Lys Glu Ser Asp Glu Val Asn Glu
865 870 875 880
Gly Glu Leu Lys Glu Ile Lys Gln Asp Ile Ser Ser Leu Arg Tyr Glu
885 890 895
Leu Leu Glu Glu Lys Ser Gln Asn Ser Glu Asp Leu Ala Glu Leu Ile
900 905 910
Arg Lys Leu Gly Glu Arg Leu Ser Leu Glu Pro Lys Leu Glu Glu Ser
915 920 925
Arg Arg
930

<210> 3
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting vector

<400> 3
tcctcaattc taactgcatt tcttctggaa aagaataaaa cgattcacca gagctccaga 60
ggatagccta agctgagttg tttttaatca aatcattctg tgtgctgtct caccccctagt 120
ttgtggctca tccaagctgt cagcaacagc tcctgtccat atggtatgag aacctctctg 180
gtttacggca gcagaccatg 200

<210> 4
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting vector

<400> 4
tcgtggtcct tgctgttgcc attggattgc ccttcctggc tctcatatac tggtgtgctc 60
cttgcagcaa ggtatgtctg tgagtcctgc agtccatctg tagttgaatt ctgtccagca 120
ggcaaagatc tagctccaaa atgaaaatat gatttgaagt acacaggttc acataatctt 180
tctatttgtt tgagaatttc 200